$\mathcal{PCT}$

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RAW SEQUENCE LISTING   DATE: 06/07/2001
PATENT APPLICATION: **US/09/830,994**   TIME: 09:22:21

Input Set : **A:\DES.txt**
Output Set: **C:\CRF3\06072001\I830994.raw** $\rho^{\mathcal{S}}$

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 3 <110> APPLICANT: YLIHONKO, Kristiina
 4         RAETY, Kaj
 5         HAKALA, Juha
 7 <120> TITLE OF INVENTION: THE GENE CLUSTER INVOLVED IN ACLACINOMYCIN BIOSYNTHESIS, AND
ITS USE FOR
 8         GENETIC ENGINEERING
10 <130> FILE REFERENCE: 1574/49884
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C--> `12 <140> CURRENT APPLICATION NUMBER: US/09/830,994`
C--> `12 <141> CURRENT FILING DATE: 2000-09-25`

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12 <150> PRIOR APPLICATION NUMBER: PCT/FI00/00819
13 <151> PRIOR FILING DATE: 2000-09-25
15 <160> NUMBER OF SEQ ID NOS: 16
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 662
21 <212> TYPE: PRT
22 <213> ORGANISM: Streptomyces galilaeus
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29 Leu Ala Pro Leu Leu Asp Gly Ser Arg Asp Leu Pro Gly Ile Val Ala
30              20                  25                  30
32 Asp Ala Ala Pro Arg Leu Pro Ala Gly Leu Ala Glu Arg Leu Val Thr
33              35                  40                  45
35 Arg Leu Leu Asp Ala Gly Leu Leu Cys Ala Tyr Pro Gln Asp Gly Ala
36         50                  55                  60
38 Asp Arg Pro Glu Arg Ala Tyr Arg Ser Leu Thr Gly Leu Gln Ala Arg
39 65                  70                  75                  80
41 Ser Ala Asp Ala Arg Asp Ala Val Leu Ala Ala Val Asp Leu Thr Gly
42                  85                  90                  95
44 Asp Ala Glu Ser Pro Leu Pro Glu Ala Val Ser Ala Ala Gly Leu Arg
45              100                 105                 110
47 Ala Ala Ala Pro Gly Glu His Ala Ala Leu Thr Leu Val Leu Cys His
48         115                 120                 125
50 Asp Tyr Leu Asp Pro Arg Leu Ser Ala Leu Asp Ala Glu His Arg Ala
51      130                 135                 140
53 Thr Gly Arg Gly Trp Leu Pro Val Arg Ala Asn Gly Thr His Leu Trp
54 145                 150                 155                 160
56 Ile Gly Pro Phe Phe Ser Ala Gly Asp Gly Pro Cys Trp Ser Cys Leu
57                  165                 170                 175
59 Ala Asp Arg Leu Arg Leu Arg Arg Arg Gly Glu Ala Tyr Val Gln His
60              180                 185                 190
62 Arg Leu Gly His Ser Gly Pro Ala Val His Arg Arg Ala Tyr Leu Pro
63              195                 200                 205
65 Ala Gly Arg Ala Ala Ala Leu Gln Leu Ala Leu Leu Glu Ala Gly Lys
66      210                 215                 220
68 Trp Leu Ser Gly His Arg Asp Thr Val Gln Asp Ser Leu Trp Arg Leu
69 225                 230                 235                 240
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ENTERED

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71 Asp Thr Arg Thr Leu Glu Ser Ser Arg His Pro Val Arg Arg Arg Pro
72                 245                 250                 255
74 Gln Cys Ser Arg Cys Gly Asp Pro Leu Leu Val Arg Asp Arg Val Ser
75             260                 265                 270
77 Ala Pro Val Val Leu Ser Ser Arg Pro Val Arg Asp Glu Ser Gly Gly
78             275                 280                 285
80 Gly His Arg Thr Phe Gly Pro Gln Glu Met Leu Asp Arg Tyr Gly His
81     290                 295                 300
83 Leu Val Asp Pro Val Thr Gly Val Val Gly Glu Ile Arg Arg Asp Pro
84 305                 310                 315                 320
86 Arg Gly Pro Glu Phe Leu Asn Cys Phe Thr Arg Ser Arg Cys Arg Leu
87             325                 330                 335
89 Gly Pro Arg Ala Ala Pro Pro Ala Leu His Ser Pro Leu Arg Ser Pro
90             340                 345                 350
92 Gly Ser Gly Lys Gly Val Thr Glu Leu His Ala Arg Val Ser Ala Leu
93             355                 360                 365
95 Ala Glu Ala Leu Glu Arg Cys Ser Gly Tyr Phe Gln Gly Asp Glu Pro
96     370                 375                 380
98 Arg Arg Arg Gly Ser Tyr Arg Glu Leu Ala Gly Leu Ala Val His Pro
99 385                 390                 395                 400
101 Asp Ser Val Gln Leu Phe Asp Arg Arg Gln Phe Glu Asp Arg Arg Ala
102                 405                 410                 415
104 Trp Asn Arg Ala His Gly Pro Phe His Gln Val Thr Glu Pro Phe Asp
105             420                 425                 430
107 Glu Asp Ala Pro Ile Asp Trp Thr Pro Val Trp Ser Leu Thr Glu Arg
108             435                 440                 445
110 Arg Gln Arg Leu Ala Pro Thr Ser Leu Leu Tyr Tyr Asn Ala Pro Asp
111     450                 455                 460
113 Ala Asp Thr Gly Phe Cys Arg Ala Thr Ser Asn Gly Ala Ala Ala Gly
114 465                 470                 475                 480
116 Thr Ser Leu Glu Asp Ala Val Val His Gly Cys Leu Glu Leu Val Glu
117             485                 490                 495
119 Arg Asp Ala Ile Ala Leu Trp Trp Tyr Asn Arg Thr Arg Gln Pro Gly
120             500                 505                 510
122 Val Thr Leu Asp Ala Arg Asp Pro Trp Ile Thr Arg Leu Arg Ala Val
123             515                 520                 525
125 Leu Arg Asp Leu Gly Arg Thr Val Trp Ala Leu Asp Leu Thr Ser Asp
126     530                 535                 540
128 Leu Gly Ile Pro Val Val Ala Ala Val Ser Val Arg Thr Gly Gly Thr
129 545                 550                 555                 560
131 Ala Glu Asp Ile Val Leu Gly Phe Gly Ala His Phe Asp Pro Arg Ile
132             565                 570                 575
134 Ala Leu Arg Arg Ala Leu Thr Glu Leu Ser Gln Met Leu Pro Pro Leu
135             580                 585                 590
137 Ala Gln Glu Thr Ala Gly Asp Ala Ser Ala Tyr Thr Gly Thr Asp Pro
138             595                 600                 605
140 Glu Ala Met Arg Trp Phe Arg His Ala Thr Thr Ala Asn Gln Pro Tyr
141     610                 615                 620
143 Leu Leu Pro Ala Ala Arg Arg Ser Ala Arg Pro Pro Ala Ser Leu Arg
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149 Arg Arg His Gly Leu Glu
150               660
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153 <211> LENGTH: 272
154 <212> TYPE: PRT
155 <213> ORGANISM: Streptomyces galilaeus
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162 Ser Ile Val Pro Thr Ala Ala Lys Pro Arg Gln Ile Leu Ala Leu Leu
163               20                   25                   30
165 Ala Ile His Ala Asn Arg Val Leu Pro Val Gly Thr Leu Met Glu Glu
166         35                   40                   45
168 Ile Trp Gly Thr Glu Pro Pro Gln Ser Ala Leu Ala Thr Leu His Thr
169      50                   55                   60
171 Tyr Ile Leu Gln Leu Arg Arg Arg Leu Thr Ala Ala Tyr Gly Asp Glu
172 65                   70                   75                   80
174 Gly Gly Val Ser Ala Lys Asp Val Leu Val Thr Gln Tyr Gly Gly Tyr
175               85                   90                   95
177 Cys Trp Gln Ala Pro Thr Asp Ser Val Asp Val Pro Arg Tyr Glu Arg
178               100                  105                  110
180 Leu Val Thr Ala Gly Arg Ile Ala Thr Ala Glu Asp Arg Gln Glu Glu
181         115                  120                  125
183 Ala Ser Ala His Phe Arg Glu Ala Leu Ala Leu Trp Arg Gly Ser Ala
184      130                  135                  140
186 Leu Val Asp Val Arg Ile Gly Pro Val Leu Ser Ile Glu Val Ala Arg
187 145                  150                  155                  160
189 Leu Glu Glu Ser Arg Leu Gly Val Leu Glu Arg Cys Leu Glu Ala Asp
190               165                  170                  175
192 Leu Arg Leu Gly Arg His Ala Glu Leu Leu Ala Glu Leu Thr Glu Leu
193               180                  185                  190
195 Thr Gly Arg His Pro Leu His Glu Gly Leu His Ala Gln Cys Met Thr
196         195                  200                  205
198 Ala Leu Tyr Arg Ala Gly Arg Ser Trp Gln Ala Leu Asp Val Tyr Gln
199      210                  215                  220
201 Arg Leu Arg Arg Arg Leu Ala Glu Glu Leu Gly Leu Ser Pro Ser Pro
202 225                  230                  235                  240
204 Arg Leu Gln Arg Leu Gln Gln Ala Val Leu Ser Ala Glu Pro Trp Leu
205               245                  250                  255
207 Asp Ala Pro Arg Tyr Gly Gly Asp Pro Val Phe Asp Arg Met Ile Ser
208               260                  265                  270
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211 <211> LENGTH: 434
212 <212> TYPE: PRT
213 <213> ORGANISM: Streptomyces galilaeus
215 <400> SEQUENCE: 3
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220 His Arg Gln Gln Gln Pro Gly Asn Phe Gln Pro Gly Val Thr Pro Ile
221             20                  25                  30
223 Leu Ser Ser Gly Ala Val Leu Asp Glu Glu Asp Arg Val Ala Leu Val
224         35                  40                  45
226 Glu Ala Ala Leu Asp Leu Arg Ile Ala Ala Gly Ala His Ser Arg Arg
227     50                  55                  60
229 Phe Glu Ser Lys Phe Ala Arg His Ile Gly Val Arg Lys Ala His Leu
230 65              70                  75                  80
232 Val Asn Ser Gly Ser Ser Ala Asn Leu Leu Ala Leu Ser Ala Leu Thr
233             85                  90                  95
235 Ser Pro Arg Leu Gly Glu Gln Arg Leu Arg Pro Gly Asp Glu Val Ile
236             100                 105                 110
238 Thr Val Ala Gly Gly Phe Pro Thr Thr Val Asn Pro Ile Leu Gln Asn
239         115                 120                 125
241 Gly Leu Thr Pro Val Phe Val Asp Leu Glu Leu Gly Thr Tyr Asn Thr
242     130                 135                 140
244 Thr Val Glu His Val Arg Ala Ala Ile Ser Asp Arg Thr Arg Ala Ile
245 145                 150                 155                 160
247 Met Ile Ala His Thr Leu Gly Asn Pro Tyr Gln Val Ala Glu Ile Gln
248             165                 170                 175
250 Gln Leu Ala Thr Glu His Glu Leu Phe Leu Ile Glu Asp Asn Cys Asp
251             180                 185                 190
253 Ala Val Gly Ser Thr Tyr Gln Gly Arg Met Thr Gly Thr Phe Gly Asp
254         195                 200                 205
256 Leu Ala Thr Val Ser Phe Tyr Pro Ala His His Ile Thr Thr Gly Glu
257     210                 215                 220
259 Gly Gly Cys Val Leu Thr Arg Asn Leu Glu Leu Ala Arg Ile Val Glu
260 225                 230                 235                 240
262 Ser Phe Arg Asp Trp Gly Arg Asp Cys Trp Cys Glu Pro Gly Glu Asp
263             245                 250                 255
265 Asn Thr Cys Leu Lys Arg Phe Asp Tyr Gln Leu Gly Asn Leu Pro Lys
266             260                 265                 270
268 Gly Tyr Asp His Lys Tyr Ile Phe Ser His Ile Gly Tyr Asn Leu Lys
269         275                 280                 285
271 Ala Thr Asp Leu Gln Gly Ala Leu Ala Leu Ser Gln Leu Asn Lys Leu
272     290                 295                 300
274 Pro Glu Phe Gly Ala Ala Arg Arg Arg Asn Trp Gln Arg Leu Arg Asp
275 305                 310                 315                 320
277 Gly Leu Ala Asp Val Pro Gly Leu Leu Leu Pro Val Ala Thr Pro Gly
278             325                 330                 335
280 Ser Asp Pro Ser Trp Phe Gly Phe Val Ile Thr Val Leu Pro Asp Ala
281             340                 345                 350
283 Thr Tyr Thr Arg Arg Asp Leu Val Ala Phe Leu Glu Glu Arg Arg Ile
284         355                 360                 365
286 Gly Thr Arg Arg Leu Phe Gly Gly Asn Leu Thr Arg His Pro Ala Tyr
287     370                 375                 380
289 Leu Gly Thr Pro His Arg Val Ala Gly Asp Leu Arg Asn Ser Asp Ile
```

```
290 385                     390                395                400
292 Ile Thr Glu Gln Ser Phe Trp Ile Gly Val Tyr Pro Gly Ile Thr Glu
293                     405                410                415
295 Glu Met Thr Asp Tyr Met Arg Glu Ser Ile Val Glu Phe Val Thr Lys
296                     420                425                430
298 Asn Gly
301 <210> SEQ ID NO: 4
302 <211> LENGTH: 329
303 <212> TYPE: PRT
304 <213> ORGANISM: Streptomyces galilaeus
306 <400> SEQUENCE: 4
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309 1                   5                  10                 15
311 Cys Ala Asp Ile Ala Val Arg Arg Ile Leu Pro Ala Ile Val Glu His
312                 20                  25                 30
314 Pro Ser Val Arg Leu Val Ala Leu Ala Ser Arg Asp Gly Ala Arg Ala
315             35                  40                 45
317 Glu Arg Leu Ala Ala Arg Phe Gly Cys Ala Ala Val Thr Gly Tyr Lys
318         50                  55                 60
320 Ala Leu Leu Asp Arg Glu Asp Ile Asn Ala Val Tyr Val Pro Leu Pro
321 65                  70                  75                 80
323 Pro Gly Met His His Glu Trp Val Thr Glu Ala Leu Thr Ala Gly Lys
324                 85                  90                 95
326 His Val Leu Val Glu Lys Pro Leu Ser Thr Thr Tyr Ala Gln Ser Val
327             100                 105                110
329 Asp Leu Val Ala Met Ala Gly Arg Leu Gly Leu Ala Leu Thr Glu Asn
330             115                 120                125
332 Phe Met Phe Leu His His Ser Gln His Glu Ala Val Arg Ala Met Thr
333         130                 135                 140
335 Gly Glu Ile Gly Glu Leu Arg Val Phe Thr Ser Ser Phe Gly Val Pro
336 145                 150                 155                160
338 Pro Pro His Pro Ser Ser Phe Arg His Asp Ala Arg Leu Gly Gly Gly
339             165                 170                175
341 Ala Leu Leu Asp Val Gly Val Tyr Pro Leu Arg Ala Ala Gln Leu His
342             180                 185                190
344 Leu Ala Gly Glu Leu Asp Val Leu Gly Ala Cys Leu Arg Val Asp Glu
345         195                 200                205
347 Ala Thr Gly Val Asp Val Ala Gly Ser Ala Leu Leu Ser Thr Ala Thr
348         210                 215                220
350 Gly Val Thr Ala Gln Leu Asp Phe Gly Phe Gln His Ala Tyr Arg Ser
351 225                 230                 235                240
353 Val Tyr Ala Leu Trp Gly Ser Arg Gly Arg Leu Ser Val Pro Arg Ala
354             245                 250                255
356 Phe Thr Pro Pro Arg Glu His Arg Pro Val Val Arg Ile Glu Gln Gln
357             260                 265                270
359 Asp Arg Leu Thr Glu Val Thr Leu Pro Ala Asp His Gln Val Gly Asn
360         275                 280                285
362 Ala Leu Asp Ala Phe Ala Ser Ala Val His Ser Glu Thr Val Arg Ala
363         290                 295                300
```

VERIFICATION SUMMARY   DATE: 06/07/2001
PATENT APPLICATION: **US/09/830,994**   TIME: 09:22:22

Input Set : **A:\DES.txt**
Output Set: **C:\CRF3\06072001\I830994.raw**

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1472 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:15
L:1485 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:16
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